

Table S1. Genes associated with disease & function pathways.

CD45⁺ cells from the brains of four WT and four *Mavs*^{-/-} mice were separated as described in Materials and Methods. RNA was purified and used in microarray analyses as described in the Results. Significance of expression differences was assessed using a false discovery rate (FDR) cutoff of 0.05 and a twofold change. Analysis and visualization of data and pathway analysis were performed using PartekGS software and Ingenuity Pathway Analysis software. There was a significant difference in expression of genes associated with disease and function pathways.